



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/070,489
Source: PCT 10
Date Processed by STIC: 3/21/02

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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Revised 01/29/2002



**Does Not Comply
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PCT10

Errors on pp.3,6-10,

13-14

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/070,489

DATE: 03/21/2002
TIME: 14:52:18

Input Set : A:\1104seq.usl
Output Set: N:\CRF3\03212002\J070489.raw

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3 <110> APPLICANT: Glare, Travis T
4      Hurst, Mark R H
5      Jackson, Trevor A
7 <120> TITLE OF INVENTION: Insecticidal nucleotide sequences
9 <130> FILE REFERENCE: sepA sepB sepC ORF1 and ORF2
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/070,489
12 <141> CURRENT FILING DATE: 2001-03-01
14 <150> PRIOR APPLICATION NUMBER: PCT/NZ00/00174
15 <151> PRIOR FILING DATE: 2000-09-04
17 <150> PRIOR APPLICATION NUMBER: NZ 337610
18 <151> PRIOR FILING DATE: 1999-09-02
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: PatentIn Ver. 2.1

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ERRORED SEQUENCES

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24 <210> SEQ ID NO: 1
25 <211> LENGTH: 18937
26 <212> TYPE: DNA
27 <213> ORGANISM: Serratia entomophila
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30 <221> NAME/KEY: CDS
31 <222> LOCATION: (2411)..(9547)
32 <223> OTHER INFORMATION: SepA
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36 <222> LOCATION: (9598)..(13884)
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40 <221> NAME/KEY: CDS
41 <222> LOCATION: (14546)..(17467)
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46 <222> LOCATION: (1860)..(2294)
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50 <221> NAME/KEY: CDS
51 <222> LOCATION: (13908)..(14483)
52 <223> OTHER INFORMATION: ORF2
54 <220> FEATURE:
55 <221> NAME/KEY: misc_feature

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RAW SEQUENCE LISTING DATE: 03/21/2002
PATENT APPLICATION: US/10/070,489 TIME: 14:52:18

Input Set : A:\1104seq.us1
Output Set: N:\CRF3\03212002\J070489.raw

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DATE: 03/21/2002
TIME: 14:52:18

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Output Set: N:\CRF3\03212002\J070489.raw

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143	ctg gtt tct ttg gtt ttt aat att ggc cag ggg aat ttt aaa cgc tct				2147
144	Leu Val Ser Leu Val Phe Asn Ile Gly Gln Gly Asn Phe Lys Arg Ser				
145	85	90	95		
147	acc ttg ttg aaa aaa ctc aac aaa cag gac tat gtc ggc gcc ggg aac				2195
148	Thr Leu Leu Lys Lys Leu Asn Lys Gln Asp Tyr Val Gly Ala Gly Asn				
149	100	105	110		
151	gag ttt tta cgc tgg acc cgg gcc aat ggg aag gtc ctt ccc gga ctg				2243
152	Glu Phe Leu Arg Trp Thr Arg Ala Asn Gly Lys Val Leu Pro Gly Leu				
153	115	120	125		
155	att cgc cga cgc gaa gct gaa cgg gtg ttg ttt gag aaa ctg ggt gca				2291
156	Ile Arg Arg Arg Glu Ala Glu Arg Val Leu Phe Glu Lys Leu Gly Ala				
157	130	135	140		
159	taa cccttgcga cgtagccaca agatgaagat aacaccgcgt actgagcggt				2344
E-->	161 145 → delete, do not place an amino acid number under a stop codon; please adjust				
163	ggcgaacaa tgaataatg actgtgtacg gcctgtcctt cacaacggat gggaccatca				2404
165	acgtaa tga atg agg caa gac att atg tat aat att gat gat att ctg				2452
166	Met Arg Gln Asp Ile Met Tyr Asn Ile Asp Asp Ile Leu				
W-->	167 150 155				
169	gag aaa gtg aat gct cca cga gca cgc ctg tca gaa gaa aac gat aca				2500
170	Glu Lys Val Asn Ala Pro Arg Ala Arg Leu Ser Glu Glu Asn Asp Thr				
W-->	171 160 165 170 175				
173	gcg gtg acg ctg acg gat tta ttc tcg cgt tcg ttt ccc gag gtc aaa				2548
174	Ala Val Thr Leu Thr Asp Leu Phe Ser Arg Ser Phe Pro Glu Val Lys				
W-->	175 180 185 190				
177	aaa atc act ggc gac agc ctg tca tgg gga gag gtc tgc tat ctg tac				2596
178	Lys Ile Thr Gly Asp Ser Leu Ser Trp Gly Glu Val Cys Tyr Leu Tyr				
W-->	179 195 200 205				
181	agt cag gcg cag cac gaa cag aaa gaa aac cgg ctc acc gaa tcc cgt				2644
182	Ser Gln Ala Gln His Glu Gln Lys Glu Asn Arg Leu Thr Glu Ser Arg				
W-->	183 210 215 220				
185	att ctg gcc cgg gcg aat ccc cta ctg gtg aat gcc gtt cgc ctg gga				2692
186	Ile Leu Ala Arg Ala Asn Pro Leu Leu Val Asn Ala Val Arg Leu Gly				
W-->	187 225 230 235				
189	ata cgg cag gca gcc ggc agt cgc agc tat gat gac tgg ttt ggc tcc				2740
190	Ile Arg Gln Ala Ala Gly Ser Arg Ser Tyr Asp Asp Trp Phe Gly Ser				
W-->	191 240 245 250 255				
193	cgc gca gac cgt ttc gcc cgc ccc ggc tcg gtg gcc tcc atg ttc tca				2788
194	Arg Ala Asp Arg Phe Ala Arg Pro Gly Ser Val Ala Ser Met Phe Ser				
W-->	195 260 265 270				
197	ccg gcg gcg tat ctg acc gag ctg tac cgt gag gcg aag gac ctg cat				2836
198	Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asp Leu His				
W-->	199 275 280 285				
201	ccg gac acc tcg ctg ttc cgg ctg gac atc cgg cgt ccc gac ctg gcg				2884
202	Pro Asp Thr Ser Leu Phe Arg Leu Asp Ile Arg Arg Pro Asp Leu Ala				
W-->	203 290 295 300				
205	gcg ctg gcc ctt agc cag aat aat atg gac gac gag ctc tcc acc ctg				2932
206	Ala Leu Ala Leu Ser Gln Asn Asn Met Asp Asp Glu Leu Ser Thr Leu				
W-->	207 305 310 315				

* Due to size of sequence, only this page shown as a sample of
numbering adjustments to be made.

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1465 accgcccgcgg gtaacggaga cgtggatatg cggatgttga ttgagctgcc ggccttaggt 18877
 1467 gtggagcgcg caaaaaatgc cggcctcgat gccctgccgg cgtgcccagc ggagcatggc 18937
 1560 <210> SEQ ID NO: 4
 1561 <211> LENGTH: 2376
 1562 <212> TYPE: PRT
 1563 <213> ORGANISM: Serratia entomophila
 1565 <220> FEATURE:
 1566 <223> OTHER INFORMATION: SepA amino acid sequence encoding an insecticidal protein

when

1567 linked with at least SEQ ID NO: 1
 1569 <400> SEQUENCE: 4
 1570 Met Arg Gln Asp Ile Met Tyr Asn Ile Asp Asp Ile Leu Glu Lys Val
 1 5 10 15
 1571 Asn Ala Pro Arg Ala Arg Leu Ser Glu Glu Asn Asp Thr Ala Val Thr
 20 25 30
 1573 Leu Thr Asp Leu Phe Ser Arg Ser Phe Pro Glu Val Lys Lys Ile Thr
 35 40 45
 1576 Gly Asp Ser Leu Ser Trp Gly Glu Val Cys Tyr Leu Tyr Ser Gln Ala
 50 55 60
 1579 Gln His Glu Gln Lys Glu Asn Arg Leu Thr Glu Ser Arg Ile Leu Ala
 65 70 75 80
 1582 Arg Ala Asn Pro Leu Leu Val Asn Ala Val Arg Leu Gly Ile Arg Gln
 85 90 95
 1585 Ala Ala Gly Ser Arg Ser Tyr Asp Asp Trp Phe Gly Ser Arg Ala Asp
 100 105 110
 1588 Arg Phe Ala Arg Pro Gly Ser Val Ala Ser Met Phe Ser Pro Ala Ala
 115 120 125
 1591 Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asp Leu His Pro Asp Thr
 130 135 140
 1594 Ser Leu Phe Arg Leu Asp Ile Arg Arg Pro Asp Leu Ala Ala Leu Ala
 145 150 155 160
 1600 Leu Ser Gln Asn Asn Met Asp Asp Glu Leu Ser Thr Leu Ser Leu Ser
 165 170 175
 1603 Asn Glu Leu Leu Tyr Arg Gly Ile Gly Ala Ala Glu Gly Leu Asp Asp
 180 185 190
 1606 Asp Ser Val Arg Glu Leu Leu Ala Gly Tyr Arg Leu Thr Gly Leu Thr
 195 200 205
 1609 Pro Tyr His Trp Ala Tyr Glu Ala Ala Arg Gln Ala Ile Leu Val Gln
 210 215 220
 1612 Asp Pro Thr Leu Met Gly Phe Ser Arg Asn Pro Asp Val Ala Gln Leu
 225 230 235 240
 1615 Met Asp Pro Ala Ser Met Leu Ala Ile Glu Ala Asp Ile Ser Pro Glu
 245 250 255
 1618 Leu Tyr Gln Ile Leu Ala Glu Glu Ile Thr Thr Asp Ser Tyr Glu Ala
 260 265 270
 1621 Leu Trp Ser Lys Asn Phe Gly Asp Met Pro Pro Ser Ser Leu Leu Ser
 275 280 285
 1624 Tyr Asp Ala Leu Ala Thr Phe Tyr Asp Leu Asp Tyr Asp Glu Leu Thr
 290 295 300
 1627 Ser Leu Leu Ser Leu Arg Leu Asp Phe Ser Asn Pro Asn Asn Glu Tyr

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1628	305	310	315	320
1630	Tyr Ile Asn Ser Gln Leu Ser Val Val Thr Leu Asn Glu Ser Thr Gly			
1631	325	330	335	
1633	Leu Ile Thr Ile His His Tyr Leu Arg Thr Leu Gly Gly Asp Ser Gln			
1634	340	345	350	
1636	Gln Ile Asn Pro Glu Leu Ile Pro Tyr Gly Asp Gly Thr Tyr Leu Tyr			
1637	355	360	365	
1639	Asn Phe Ser Val Val Ser Thr Ile Ser Glu Asp Ser Phe Lys Leu Gly			
1640	370	375	380	
1642	Ser Leu Gly Ser Asn Ser Asn Leu Tyr Ser Gly Asp Tyr Gln Leu			
1643	385	390	395	400
1645	Gln Lys Gly Val Arg Tyr Ser Ile Pro Val Glu Ile Asp Glu Gly Lys			
1646	405	410	415	
1648	Leu Asn Asp Gly Ile Thr Ile Gly Leu Ser Arg Lys Gly Gly Tyr			
1649	420	425	430	
1651	Tyr Ser Thr Val Asn Phe Thr Leu Ile Glu Tyr Asp Pro Ala Ile Phe			
1652	435	440	445	
1654	Ile Leu Lys Leu Asn Lys Val Ile Arg Leu Tyr Lys Ala Thr Gly Met			
1655	450	455	460	
1657	Thr Thr Ala Glu Ile Tyr Gln Ile Thr Asn Ile Leu Asn Asn Gly Leu			
1658	465	470	475	480
1660	Thr Ile Asp His Ala Val Leu Ser Lys Ile Phe Leu Val Arg Tyr Leu			
1661	485	490	495	
1663	Met Arg His Tyr Gln Leu Asp Val Ala Arg Ser Leu Ile Leu Cys Asn			
1664	500	505	510	
1666	Gly Thr Ile Ser Asp Gln Ala Phe Ser Gly Glu Thr Gly Leu Phe Thr			
1667	515	520	525	
1669	Thr Leu Phe Asn Thr Pro Pro Leu Asn Gly Gln Leu Phe Ser Ala Asp			
1670	530	535	540	
1672	Asp Thr Pro Leu Asp Leu Arg Ser Glu Ala Pro Glu Asp Ala Phe Arg			
1673	545	550	555	560
1675	Leu Ser Val Leu Lys Arg Ala Phe Asn Ile Ser Ala Ser Gly Leu Ser			
1676	565	570	575	
1678	Thr Leu Trp Gln Leu Ala Ser Gly Asp Ser Ser Ala Gly Phe Ser Cys			
1679	580	585	590	
1681	Ser Ala Asp Asn Ile Ala Ala Leu Tyr Arg Val Lys Leu Leu Ala Asp			
1682	595	600	605	
1684	Ile His Asp Leu Ser Ala Gly Glu Leu Ser Met Leu Leu Ser Val Ser			
1685	610	615	620	
1687	Pro Phe Ser Gly Val Ala Ala Gly Ser Leu Ser Asp Asn Glu Leu Thr			
1688	625	630	635	640
1690	Gln Phe Leu Tyr Gln Thr Thr Trp Leu Thr Glu Gln Gly Trp Thr			
1691	645	650	655	
1693	Val Ser Asp Val Phe Leu Met Leu Thr Thr Gln Tyr Gly Thr Leu Leu			
1694	660	665	670	
1696	Thr Pro Asp Ile Glu Asn Leu Leu Ala Ser Leu Arg Asn Gly Leu Ser			
1697	675	680	685	
1699	Gly Arg Glu Leu Phe Pro Glu Thr Leu Pro Gly Asp Gly Ala Pro Phe			
1700	690	695	700	

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1702	Ile Ala Ala Ala Met Gln Leu Asp Ala Thr Asp Thr Ala Lys Ala Met			
1703	705	710	715	720
1705	Leu Thr Trp Ala Asp Gln Leu Lys Pro Glu Gly Leu Thr Leu Thr Glu			
1706	725	730	735	
1708	Phe Ile Leu Leu Val Met Asn Ala Ala Pro Asn Asp Glu Gln Ala Gly			
1709	740	745	750	
1711	Gln Met Ala Gly Phe Cys Gln Ala Leu Trp Gln Leu Ala Leu Ile Ile			
1712	755	760	765	
1714	Arg Ser Thr Gly Leu Ser Thr Arg Glu Leu Thr Leu Leu Val Ser Gln			
1715	770	775	780	
1717	Pro Gly Arg Phe Arg Thr Gly Trp His His Leu Pro His Asp Leu Pro			
1718	785	790	795	800
1720	Ala Leu Arg Asp Ile Thr Arg Phe His Ala Val Val Asn Arg Ser Gly			
1721	805	810	815	
1723	Ser His Ala Gly Glu Val Leu Thr Ala Leu Glu Thr Gly Glu Leu Ser			
1724	820	825	830	
1726	Ser Ala Leu Leu Ala Arg Ala Leu Ser Gln Asn Glu Gln Asp Val Thr			
1727	835	840	845	
1729	Gly Ala Leu Ala Gln Val Arg Gly Ala Gly Glu Gln Asp Asn Ser Val			
1730	850	855	860	
1732	Phe Thr Ser Trp Glu Glu Val Asp Gln Ala Glu Gln Trp Leu Asp Met			
1733	865	870	875	880
1735	Ser Glu Thr Leu Ser Ile Thr Pro Ser Gly Leu Ala Ser Leu Ile Ala			
1736	885	890	895	
1738	Leu Lys Tyr Ile Asn Val Ser Asp Asp Ser Ala Pro Leu Tyr Ser Gln			
1739	900	905	910	
1741	Trp Gln Val Val Ser Gly Leu Leu Gln Ala Gly Leu Lys Ser Ser Gln			
1742	915	920	925	
1744	Ser Ser Ala Leu His Asp Tyr Leu Glu Glu Gly Thr Ser Ser Ala Leu			
1745	930	935	940	
1747	Cys Ala Tyr Tyr Leu Arg Asn Leu Ala Pro Asn Met Val Ser Gly Arg			
1748	945	950	955	960
1750	Asp Asp Leu Phe Gly Tyr Leu Leu Leu Asp Asn Gln Val Ser Ala Lys			
1751	965	970	975	
1753	Val Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Gly Ile Arg Leu Tyr			
1754	980	985	990	
1756	Ile Asn Arg Ala Leu Asn Gly Ile Glu Leu Ser Ala Met Ala Glu Val			
1757	995	1000	1005	
1759	Arg Gly Arg Gln Phe Phe Thr Asp Trp Asp Thr Phe Asn Lys Arg Tyr			
1760	1010	1015	1020	
1762	Ser Thr Trp Ala Gly Val Ser Glu Leu Val Tyr Tyr Pro Glu Asn Tyr			
E--> 1763	025	1030	1035	1040
1765	Leu Asp Pro Thr Val Arg Ile Gly Gln Thr Gly Met Met Asp Thr Leu			
1766	1045	1050	1055	
1768	Leu Gln Ser Val Ser Gln Ser Ser Ile Asn Arg Asp Thr Val Glu Asp			
1769	1060	1065	1070	
1771	Ala Phe Lys Thr Tyr Leu Thr Thr Phe Glu Gln Ile Ala Asn Leu Asn			
1772	1075	1080	1085	
1774	Thr Val Ser Gly Tyr His Asp Asn Ala Ser Met Thr Gln Gly Thr Thr			

Please align the first digit (1 in 1025) immediately underneath the first letter of the first amino acid appearing in a line. Some error repeated throughout this sequence and the next sequence.

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1775	1090	1095	1100
1777	Trp Tyr Val Gly Arg Ser Ile Thr Asp Gln Thr Asn Trp Tyr Trp Arg		
E--> 1778	105	1110	1115
1780	Ser Ala Asn His Ser Lys Ile Gln Asp Ser Met Met Pro Ala Asn Ala		1120
1781	1125	1130	1135
1783	Trp Thr Gly Trp Thr Lys Ile Asn Cys Gly Met Asn Pro Trp Ser Asp		
1784	1140	1145	1150
1786	Leu Val Cys Ser Val Phe Phe Asn Ser Arg Leu Tyr Val Val Trp Val		
1787	1155	1160	1165
1789	Glu Glu Asn Gln Ser Ala Asp Thr Glu Ala Glu Ser Thr Thr Thr		
1790	1170	1175	1180
1792	Gln Gln Ser Tyr Thr Leu Lys Leu Ser Phe Arg Arg Tyr Asp Gly Thr		
E--> 1793	185	1190	1195
1795	Trp Ser Ser Pro Val Ser Phe Asp Ile Thr Gly Asn Ile Ala Phe Pro		1200
1796	1205	1210	1215
1798	Glu Thr Gln Gly Met His Val Thr Cys Asn Pro Leu Thr Glu Gln Leu		
1799	1220	1225	1230
1801	Tyr Cys Ala Phe Tyr Ser Val Thr Ser Lys Pro Asp Phe Asp Asn Ala		
1802	1235	1240	1245
1804	Gln Leu Ile Ser Val Asp Asn Asp Met Thr Leu Asn Val Ile Ser Asp		
1805	1250	1255	1260
1807	Ile Gly Ile Phe Lys Ser Val Ser His Glu Phe Asn Thr Ser Thr Glu		
E--> 1808	265	1270	1275
1810	Lys Phe Ile Asn Asn Val Phe Ser Asp Pro Ser Ala Asn Tyr Phe Val		1280
1811	1285	1290	1295
1813	Ser Ala Thr Ser Leu Ile Asp Asp Val Ile His Ser Asp Phe Ser Leu		
1814	1300	1305	1310
1816	Leu Asn Ser Lys Thr Thr Ser Thr Val Phe Thr Asn Glu Asp Ser Ser		
1817	1315	1320	1325
1819	Leu Leu Thr Pro Glu Leu His Ile Thr Ala Asn Val Ser Cys Phe Val		
1820	1330	1335	1340
1822	Ser Thr Ala Gly Ile Ala Thr Gln Ser Thr Ile Glu Lys Phe Val Gln		
E--> 1823	345	1350	1355
1825	Ala Gly Ile Glu Phe Glu Glu Ile Asn Phe Tyr Ala Gly Gln Ala Ala		1360
1826	1365	1370	1375
1828	Gly Gly Phe Asp Gly Phe Val Gly Val Asp Val Ser Asn Ser Lys Val		
1829	1380	1385	1390
1831	Tyr Gln Val Gly Lys Glu Ala Val Gly Val Thr Val Lys Ser Tyr Ser		
1832	1395	1400	1405
1834	Val Thr Gly Val Ser Gly Ser Val Glu Leu Phe Ile Asp Ser Ser Asn		
1835	1410	1415	1420
1837	Lys Tyr Phe Ser Gly Ile Leu Ser Asp Lys Met Ile Thr Ala Leu Ile		
E--> 1838	425	1430	1435
1840	Ser Gly Ser Thr Ser Lys Val Asn Tyr Val Ser Ser Ile Gly Ser Gln		1440
1841	1445	1450	1455
1843	Asp Phe Trp Ser Val Lys Ser Leu Met Pro Ala Leu Gln Ile Tyr Glu		
1844	1460	1465	1470
1846	Leu Ile Asp Asp Ile Ile Leu Thr Ser Gly Val Asn Gly Thr Glu Ile		
1847	1475	1480	1485

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1849 Lys Ser Trp Pro Ser Ala Glu Trp Tyr Asn Asp Lys Leu Ser Leu Gln
1850 1490 1495 1500
1852 Ser Gly Asn Asn Leu Phe Asn Thr Lys Ser Leu Ser Phe Thr Val Asn
E--> 1853 505 1510 1515 1520
1855 Thr Ser Asp Ile Val Glu Asp Glu Phe Asp Val Thr Phe Thr Phe Thr
1856 1525 1530 1535
1858 Ala Val Asp Gln Asn Asn Val Val Leu Ala Ala Arg Thr Ala Ile Leu
1859 1540 1545 1550
1861 Thr Val Ile Arg Asn Ile Asn Asn Asp Thr Ser Val Ile Ala Leu Arg
1862 1555 1560 1565
1864 Lys Asn Thr Arg Gly Ala Gln Tyr Ile Arg Phe Thr Ala Gly Asn Asp
1865 1570 1575 1580
1867 Val Ala Leu Ile Arg Leu Asn Thr Leu Phe Ala Arg Gln Leu Val Asp
E--> 1868 585 1590 1595 1600
1870 Arg Ala Asn Thr Gly Ile Asp Thr Ile Leu Ser Met Glu Thr Gln Arg
1871 1605 1610 1615
1873 Leu Thr Glu Pro Ala Leu Glu Glu Gly Ser Asp Val Phe Met Asp Phe
1874 1620 1625 1630
1876 Ser Gly Ala Asn Ala Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro
1877 1635 1640 1645
1879 Met Met Val Phe Gln Arg Leu Leu Gln Glu Gln His Phe Pro Glu Ala
1880 1650 1655 1660
1882 Thr Arg Trp Leu Gln Tyr Val Trp Asn Pro Ala Gly His Val Val Asn
E--> 1883 665 1670 1675 1680
1885 Gly Val Leu Gln Asn Tyr Thr Trp Asn Val Arg Pro Leu Glu Glu Asp
1886 1685 1690 1695
1888 Thr Gly Trp Asn Asp Ser Pro Leu Asp Ser Ile Asp Pro Asp Ala Ile
1889 1700 1705 1710
1891 Ala Gln Tyr Asp Pro Met His Tyr Lys Val Ala Thr Phe Met Ser Tyr
1892 1715 1720 1725
1894 Leu Asp Leu Leu Ile Ala Arg Gly Asp Ala Ala Tyr Arg Leu Leu Glu
1895 1730 1735 1740
1897 Arg Asp Thr Leu Asn Glu Ala Arg Met Trp Tyr Val Gln Ala Leu Asn
E--> 1898 745 1750 1755 1760
1900 Leu Leu Gly Asp Glu Pro Tyr Ile Ser Phe Asp Ala Asp Trp Ser Ala
1901 1765 1770 1775
1903 Leu Thr Leu Gly Asp Ala Ala Ser Glu Val Thr Arg Arg Asp Tyr Gln
1904 1780 1785 1790
1906 Glu Ala Leu Leu Ala Val Arg Arg Leu Val Pro Ala Pro Glu Thr Arg
1907 1795 1800 1805
1909 Thr Ala Asn Ser Leu Thr Ala Leu Phe Leu Pro Gln Gln Asn Glu Val
1910 1810 1815 1820
1912 Leu Lys Gly Tyr Trp Gln Thr Leu Ala Gln Arg Leu His Asn Leu Arg
E--> 1913 825 1830 1835 1840
1915 His Asn Leu Ser Ile Asp Gly Gln Pro Leu Ser Leu Ser Val Tyr Ala
1916 1845 1850 1855
1918 Thr Pro Ser Glu Pro Ser Ala Leu Gln Ser Ala Val Val Asn Ser Ala
1919 1860 1865 1870
1921 Gln Gly Ala Ala Ala Leu Pro Ala Ala Val Met Pro Leu Tyr Ser Phe

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1922	1875	1880	1885
1924	Pro Val Met Leu Glu Asn Ala Arg Gly Met Val Ser Leu Leu Thr Gly		
1925	1890	1895	1900
1927	Phe Gly Asn Thr Leu Leu Gly Ile Thr Glu Arg Gln Asp Ala Glu Ala		
E--> 1928	905	1910	1915
			1920
1930	Leu Ala Lys Leu Leu Gln Thr Gln Gly Ser Glu Leu Ile Arg Gln Gly		
1931	1925	1930	1935
1933	Leu Arg Gln Gln Asp Asn Val Leu Glu Ile Asp Ala Asp Ile Ala		
1934	1940	1945	1950
1936	Ala Leu Glu Glu Ser Arg Arg Gly Ala Gln Met Arg Phe Glu Arg Tyr		
1937	1955	1960	1965
1939	Lys Val Leu Tyr Glu Ala Asp Val Asn Thr Gly Glu Lys Gln Ala Met		
1940	1970	1975	1980
1942	Asp Leu Tyr Leu Ser Ser Val Leu Ser Ala Ser Thr Ala Ala Leu		
E--> 1943	985	1990	1995
			2000
1945	Phe Leu Ala Glu Ala Ala Asp Met Leu Pro Asn Ile Tyr Gly Leu		
1946	2005	2010	2015
1948	Ala Val Gly Gly Ser Arg Tyr Gly Ala Leu Phe Lys Ala Thr Ala Ile		
1949	2020	2025	2030
1951	Gly Ile Gln Val Ser Ser Asp Ala Thr Arg Ile Ser Ala Asp Lys Ile		
1952	2035	2040	2045
1954	Ser Gln Ser Glu Val Tyr Arg Arg Arg Glu Glu Trp Glu Ile Gln		
1955	2050	2055	2060
1957	Arg Asp Ser Ala Gln Ser Asp Val Ala Gln Ile Asp Ala Gln Leu Ala		
E--> 1958	065	2070	2075
			2080
1960	Ala Met Ala Val Arg Arg Glu Gly Ala Glu Leu Gln Lys Thr Tyr Leu		
1961	2085	2090	2095
1963	Glu Thr Gln Gln Thr Gln Ala Gln Ala Gln Leu Ala Phe Leu Gln Ser		
1964	2100	2105	2110
1966	Lys Phe Asn Asn Thr Ala Leu Tyr Ser Trp Leu Arg Gly Arg Leu Ser		
1967	2115	2120	2125
1969	Ala Ile Tyr Tyr Gln Phe Tyr Asp Leu Ala Val Ser Arg Cys Leu Met		
1970	2130	2135	2140
1972	Ala Gln Gln Ala Trp Gln Trp Asp Lys Phe Glu Thr Arg Ser Phe Ile		
E--> 1973	145	2150	2155
			2160
1975	Gln Pro Gly Ala Trp Met Gly Ala Asn Ala Gly Leu Leu Ala Gly Glu		
1976	2165	2170	2175
1978	Thr Leu Met Leu Asn Leu Ala Gln Met Glu Gln Ala Trp Leu Thr Gly		
1979	2180	2185	2190
1981	Asp Glu Arg Ala Ile Glu Val Thr Arg Thr Val Cys Leu Ser Glu Val		
1982	2195	2200	2205
1984	Tyr Thr Ser Leu Ala Glu Asp Ala Ala Phe Ser Leu Ala Asp Lys Val		
1985	2210	2215	2220
1987	Val Glu Leu Val Ser Asn Gly Ser Gly Ser Ala Gly Thr Lys Ser Asn		
E--> 1988	225	2230	2235
			2240
1990	Gly Leu Gln Met Asp Gln Gln Leu Glu Ala Thr Leu Lys Leu Ala		
1991	2245	2250	2255
1993	Asp Leu Gly Ile Gly Asn Asp Tyr Pro Val Ser Leu Gly Thr Met Arg		
1994	2260	2265	2270

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Input Set : A:\1104seq.usl
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1996 Arg Ile Lys Gln Ile Ser Val Thr Leu Pro Ala Leu Val Gly Pro Tyr
1997 2275 2280 2285
1999 Gln Asp Val Arg Ala Val Leu Ser Tyr Gly Gly Ser Met Val Met Pro
2000 2290 2295 2300
2002 Arg Gly Cys Ser Ala Leu Ala Val Ser His Gly Met Asn Asp Ser Gly
E--> 2003 305 2310 2315 2320
2005 Gln Phe Gln Leu Asp Phe Asn Asp Pro Arg Tyr Leu Pro Phe Glu Gly
2006 2325 2330 2335
2008 Leu Pro Val Asp Asp Thr Gly Thr Leu Thr Leu Ser Phe Pro Asp Ala
2009 2340 2345 2350
2011 Asp Gly Lys Gln Gln Ala Met Leu Leu Ser Leu Ser Asp Ile Ile Leu
2012 2355 2360 2365
2014 His Ile Arg Tyr Thr Ile Ile Ser
2015 2370 2375
2019 <210> SEQ ID NO: 5
2020 <211> LENGTH: 1428
2021 <212> TYPE: PRT
2022 <213> ORGANISM: Serratia entomophila
2024 <220> FEATURE:
2025 <223> OTHER INFORMATION: SepB amino acid sequence encoding an insecticidal protein

when

2026 linked with at least SEQ ID NO: 1
2028 <400> SEQUENCE: 5
2029 Met Gln Asn His Gln Asp Met Ala Ile Thr Ala Pro Thr Leu Pro Ser
2030 1 5 10 15
2032 Gly Gly Gly Ala Val Thr Gly Leu Lys Gly Asp Ile Ala Ala Ala Gly
2033 20 25 30
2035 Pro Asp Gly Ala Ala Thr Leu Ser Ile Pro Leu Pro Val Ser Pro Gly
2036 35 40 45
2038 Arg Gly Tyr Ala Pro Thr Gly Ala Leu Asn Tyr His Ser Arg Ser Gly
2039 50 55 60
2041 Asn Gly Pro Phe Gly Ile Gly Trp Gly Ile Gly Ala Ala Val Gln
2042 65 70 75 80
2044 Arg Arg Thr Arg Asn Gly Ala Pro Thr Tyr Asp Asp Thr Asp Glu Phe
2045 85 90 95
2047 Thr Gly Pro Asp Gly Glu Val Leu Val Pro Ala Leu Thr Ala Ala Gly
2048 100 105 110
2050 Thr Gln Glu Ala Arg Gln Ala Thr Ser Leu Leu Gly Ile Asn Pro Gly
2051 115 120 125
2053 Gly Ser Phe Asn Val Gln Val Tyr Arg Ser Arg Thr Glu Gly Ser Leu
2054 130 135 140
2056 Ser Arg Leu Glu Arg Trp Leu Pro Ala Asp Glu Thr Glu Thr Glu Phe
2057 145 150 155 160
2059 Trp Val Leu Tyr Thr Pro Asp Gly Gln Val Ala Leu Leu Gly Arg Asn
2060 165 170 175
2062 Ala Gln Ala Arg Ile Ser Asn Pro Thr Ala Pro Thr Gln Thr Ala Val
2063 180 185 190
2065 Trp Leu Met Glu Ser Ser Val Ser Leu Thr Gly Glu Gln Met Tyr Tyr
2066 195 200 205
2068 Gln Tyr Arg Ala Glu Asp Asp Gly Cys Asp Glu Ala Glu Arg Asp

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2069	210	215	220
2071	Ala His Pro Gln Ala Gly Ala Gln Arg Tyr Pro Val Ala Val Trp Tyr		
2072	225	230	235
2074	Gly Asn Arg Gln Ala Ala Arg Thr Leu Pro Ala Leu Val Ser Thr Pro		240
2075	245	250	255
2077	Ser Met Asp Ser Trp Leu Phe Ile Leu Val Phe Asp Tyr Gly Glu Arg		
2078	260	265	270
2080	Ser Ser Val Leu Ser Glu Ala Pro Ala Trp Gln Thr Pro Gly Ser Gly		
2081	275	280	285
2083	Glu Trp Leu Cys Arg Gln Asp Cys Phe Ser Gly Tyr Glu Phe Gly Phe		
2084	290	295	300
2086	Asn Leu Arg Thr Arg Arg Leu Cys Arg Gln Val Leu Met Phe His Tyr		
2087	305	310	315
2089	Leu Gly Val Leu Ala Gly Ser Ser Gly Ala Asn Asp Ala Pro Ala Leu		320
2090	325	330	335
2092	Ile Ser Arg Leu Leu Leu Asp Tyr Arg Glu Ser Pro Ser Leu Ser Leu		
2093	340	345	350
2095	Leu Glu Asn Val His Gln Val Ala Tyr Glu Ser Asp Gly Thr Ser Cys		
2096	355	360	365
2098	Ala Leu Pro Ala Leu Ala Leu Gly Trp Gln Thr Phe Thr Pro Pro Thr		
2099	370	375	380
2101	Leu Ser Ala Trp Gln Thr Arg Asp Asp Met Gly Lys Leu Ser Leu Leu		
2102	385	390	395
2104	Gln Pro Tyr Gln Leu Val Asp Leu Asn Gly Glu Gly Val Val Gly Ile		400
2105	405	410	415
2107	Leu Tyr Gln Asp Ser Gly Ala Trp Trp Tyr Arg Glu Pro Val Arg Gln		
2108	420	425	430
2110	Ser Gly Asp Asp Pro Asp Ala Val Thr Trp Gly Ala Ala Ala Leu		
2111	435	440	445
2113	Pro Thr Met Pro Ala Leu His Asn Ser Gly Ile Leu Ala Asp Leu Asn		
2114	450	455	460
2116	Gly Asp Gly Arg Leu Glu Trp Val Val Thr Ala Pro Gly Val Ala Gly		
2117	465	470	475
2119	Met Tyr Asp Arg Thr Pro Gly Arg Asp Trp Leu His Phe Thr Pro Leu		480
2120	485	490	495
2122	Ser Ala Leu Pro Val Glu Tyr Ala His Pro Lys Ala Val Leu Ala Asp		
2123	500	505	510
2125	Ile Leu Gly Ala Gly Leu Thr Asp Met Val Leu Ile Gly Pro Arg Ser		
2126	515	520	525
2128	Val Arg Leu Tyr Ser Gly Lys Asn Asp Gly Trp Asn Lys Gly Glu Thr		
2129	530	535	540
2131	Val Gln Gln Thr Glu Arg Leu Thr Leu Pro Val Pro Gly Val Asp Pro		
2132	545	550	555
2134	Arg Thr Leu Val Ala Phe Ser Asp Met Ala Gly Ser Gly Gln Gln His		560
2135	565	570	575
2137	Leu Thr Glu Val Arg Ala Asn Gly Val Arg Tyr Trp Pro Asn Leu Gly		
2138	580	585	590
2140	His Gly Arg Phe Gly Gln Pro Val Asn Ile Pro Gly Phe Ser Gln Ser		
2141	595	600	605

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Input Set : A:\1104seq.usl
Output Set: N:\CRF3\03212002\J070489.raw

2143 Val Thr Thr Phe Asn Pro Asp Gln Ile Leu Leu Ala Asp Thr Asp Gly
 2144 610 615 620
 2146 Ser Gly Thr Thr Asp Leu Ile Tyr Ala Met Ser Asp Arg Leu Val Ile
 2147 625 630 635 640
 2149 Tyr Phe Asn Gln Ser Gly Asn Tyr Phe Ala Glu Pro His Thr Leu Leu
 2150 645 650 655
 2152 Leu Pro Lys Gly Val Arg Tyr Asp Arg Thr Cys Ser Leu Gln Val Ala
 2153 660 665 670
 2155 Asp Ile Gln Gly Leu Gly Val Pro Ser Leu Leu Leu Thr Val Pro His
 2156 675 680 685
 2158 Val Ala Pro His His Trp Val Cys His Leu Ser Ala Asp Lys Pro Trp
 2159 690 695 700
 2161 Leu Leu Asn Gly Met Asn Asn Asn Met Gly Ala Arg His Ala Leu His
 2162 705 710 715 720
 2164 Tyr Arg Ser Ser Val Gln Phe Trp Leu Asp Glu Lys Ala Glu Ala Leu
 2165 725 730 735
 2167 Ala Ala Gly Ser Ser Pro Ala Cys Tyr Leu Pro Phe Thr Leu His Thr
 2168 740 745 750
 2170 Leu Trp Arg Ser Val Val Gln Asp Glu Ile Thr Gly Asn Arg Leu Val
 2171 755 760 765
 2173 Ser Asp Val Leu Tyr Arg His Gly Val Trp Asp Gly Gln Glu Arg Glu
 2174 770 775 780
 2176 Phe Arg Gly Phe Gly Phe Val Glu Ile Arg Asp Thr Asp Thr Leu Ala
 2177 785 790 795 800
 2179 Ser Gln Gly Thr Ala Thr Glu Leu Ser Met Pro Ser Val Ser Arg Asn
 2180 805 810 815
 2182 Trp Tyr Ala Thr Gly Val Pro Ala Val Asp Glu Arg Leu Pro Glu Thr
 2183 820 825 830
 2185 Tyr Trp Gln Asn Asp Ala Ala Ala Phe Ala Asp Phe Ala Thr Arg Phe
 2186 835 840 845
 2188 Thr Val Gly Ser Gly Glu Asp Glu Gln Thr Tyr Thr Pro Asp Asp Ser
 2189 850 855 860
 2191 Lys Thr Phe Trp Leu Gln Arg Ala Leu Lys Gly Ile Leu Leu Arg Ser
 2192 865 870 875 880
 2194 Glu Leu Tyr Gly Ala Asp Gly Ser Ser Gln Ala Asp Ile Pro Tyr Ser
 2195 885 890 895
 2197 Val Thr Glu Ser Arg Pro Gln Val Arg Leu Val Glu Ala Asn Gly Asp
 2198 900 905 910
 2200 Tyr Pro Val Val Trp Pro Met Gly Ala Glu Ser Arg Thr Ser Val Tyr
 2201 915 920 925
 2203 Glu Arg Tyr His Asn Asp Pro Gln Cys Gln Gln Gln Ala Val Leu Leu
 2204 930 935 940
 2206 Ser Asp Glu Tyr Gly Phe Pro Leu Arg Gln Val Ser Val Asn Tyr Pro
 2207 945 950 955 960
 2209 Arg Arg Pro Pro Ser Ala Asp Asn Pro Tyr Pro Ala Ser Leu Pro Ala
 2210 965 970 975
 2212 Thr Leu Phe Ala Asn Ser Tyr Asp Glu Gln Gln Gln Ile Leu Arg Leu
 2213 980 985 990
 2215 Gly Leu Gln Gln Ser Ser Ala His His Leu Val Ser Leu Ser Glu Gly

Please see explanation on p. 6. Same error.

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Input Set : A:\1104seq.usl
Output Set: N:\CRF3\03212002\J070489.raw

2216	995	1000	1005
2218	His Trp Leu Leu Gly Leu Ala Glu Ala Ser Arg Asp Asp Val Phe Thr		
2219	1010	1015	1020
2221	Tyr Ser Ala Asp Asn Val Pro Glu Gly Gly Leu Thr Leu Glu His Leu		
E--> 2222	025	1030	1035
2224	Leu Ala Pro Glu Ser Leu Val Ser Asp Ser Gln Val Gly Thr Leu Ala		
2225	1045	1050	1055
2227	Gly Gln Gln Gln Val Trp Tyr Leu Asp Ser Gln Asp Val Ala Thr Val		
2228	1060	1065	1070
2230	Ala Ala Pro Pro Leu Pro Pro Lys Val Ala Phe Ile Glu Thr Ala Val		
2231	1075	1080	1085
2233	Leu Asp Glu Gly Met Val Ser Ser Leu Ala Ala Tyr Ile Val Asp Glu		
2234	1090	1095	1100
2236	His Leu Glu Gln Ala Gly Tyr Arg Gln Ser Gly Tyr Leu Phe Pro Arg		
E--> 2237	105	1110	1115
2239	Gly Arg Glu Ala Glu Gln Ala Leu Trp Thr Gln Cys Gln Gly Tyr Val		
2240	1125	1130	1135
2242	Thr Tyr Ala Gly Ala Glu His Phe Trp Leu Pro Leu Ser Phe Arg Asp		
2243	1140	1145	1150
2245	Ser Met Leu Thr Gly Pro Val Thr Val Thr Arg Asp Ala Tyr Asp Cys		
2246	1155	1160	1165
2248	Val Ile Thr Gln Trp Gln Asp Ala Ala Gly Ile Val Thr Thr Ala Asp		
2249	1170	1175	1180
2251	Tyr Asp Trp Arg Phe Leu Thr Pro Val Arg Val Thr Asp Pro Asn Asp		
E--> 2252	185	1190	1195
2254	Asn Leu Gln Ser Val Thr Leu Asp Ala Leu Gly Arg Val Thr Thr Leu		
2255	1205	1210	1215
2257	Arg Phe Trp Gly Thr Glu Asn Gly Ile Ala Thr Gly Tyr Ser Asp Ala		
2258	1220	1225	1230
2260	Thr Leu Ser Val Pro Asp Gly Ala Ala Ala Leu Ala Leu Thr Ala		
2261	1235	1240	1245
2263	Pro Leu Pro Val Ala Gln Cys Leu Val Tyr Val Thr Asp Ser Trp Gly		
2264	1250	1255	1260
2266	Asp Asp Asp Asn Glu Lys Met Pro Pro His Val Val Val Leu Ala Thr		
E--> 2267	265	1270	1275
2269	Asp Arg Tyr Asp Ser Asp Thr Gly Gln Gln Val Arg Gln Gln Val Thr		
2270	1285	1290	1295
2272	Phe Ser Asp Gly Phe Gly Arg Glu Leu Gln Ser Ala Thr Arg Gln Ala		
2273	1300	1305	1310
2275	Glu Gly Asn Ala Trp Gln Arg Gly Arg Asp Gly Lys Leu Val Thr Ala		
2276	1315	1320	1325
2278	Ser Asp Gly Leu Pro Val Thr Val Ala Thr Asn Phe Arg Trp Ala Val		
2279	1330	1335	1340
2281	Thr Gly Arg Ala Glu Tyr Asp Asn Lys Gly Leu Pro Val Arg Val Tyr		
E--> 2282	345	1350	1355
2284	Gln Pro Tyr Phe Leu Asp Ser Trp Gln Tyr Val Ser Asp Asp Ser Ala		
2285	1365	1370	1375
2287	Arg Gln Asp Leu Tyr Ala Asp Thr His Phe Tyr Asp Pro Thr Ala Arg		
2288	1380	1385	1390

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Input Set : A:\1104seq.usl
Output Set: N:\CRF3\03212002\J070489.raw

2290 Glu Trp Gln Val Ile Thr Ala Lys Gly Glu Arg Arg Gln Val Leu Tyr
2291 1395 1400 1405
2293 Thr Pro Trp Phe Val Val Ser Glu Asp Glu Asn Asp Thr Val Gly Leu
2294 1410 1415 1420
2296 Asn Asp Ala Ser
E--> 2297 425

VERIFICATION SUMMARY
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Input Set : A:\1104seq.us1
Output Set: N:\CRF3\03212002\J070489.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:161 M:254 E: No. of Bases conflict, LENGTH:Input:145 Counted:2344 SEQ:1
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:275 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:311 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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Input Set : A:\1104seq.us1

Output Set: N:\CRF3\03212002\J070489.raw

L:351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:1763 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:2222 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5